

## Sequences

[0087] <120> PEG-conjugates of NK4

<130> Case 20859

<140>

<141>

<150> 01104640.6

<151> 2001-02-23

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1344)

<400> 1

caa agg aaa aga aga aat aca att cat gaa ttc aaa aaa tca gca aag 48

Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys

1

5

10

15

act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa aaa 96

Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys

20

25

30

gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa gga	144
Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly	
35 40 45	
ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa caa	192
Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln	
50 55 60	
tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa gaa	240
Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu	
65 70 75 80	
ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga aac	288
Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn	
85 90 95	
tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc act	336
Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr	
100 105 110	
aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac gaa	384
Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu	
115 120 125	
cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa aac	432
His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn	
130 135 140	
tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc aca	480
Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr	
145 150 155 160	
agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt tca	528
Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser	
165 170 175	

gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt ctc atg 576  
 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met  
 180 185 190

gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat cag aca 624  
 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr  
 195 200 205

cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag ggc ttt 672  
 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe  
 210 215 220

gat gat aat tat tgc cgc aat ccc gat ggc cag ccg agg cca tgg tgc 720  
 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys  
 225 230 235 240

tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa aca 768  
 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr  
 245 250 255

tgc gct gac aat act atg aat gac act gat gtt cct ttg gaa aca act 816  
 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr  
 260 265 270

gaa tgc atc caa ggt caa gga gaa ggc tac agg ggc act gtc aat acc 864  
 Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr  
 275 280 285

att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat cct cac 912  
 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His  
 290 295 300

gag cat gac atg act cct gaa aat ttc aag tgc aag gac cta cga gaa 960  
 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu  
 305 310 315 320

aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt ttt acc 1008  
 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr  
 325 330 335

act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca aac tgt 1056  
 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys  
 340 345 350

gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa aat tat 1104  
 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr  
 355 360 365

atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg tgg 1152  
 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp  
 370 375 380

gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa cca gat 1200  
 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp  
 385 390 395 400

gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat gct 1248  
 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala  
 405 410 415

cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat tat 1296  
 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr  
 420 425 430

tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca ata gtc taa 1344  
 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
 435 440 445

<210> 2

<211> 447

<212> PRT

<213> Homo sapiens

<400> 2

Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys  
1 5 10 15  
Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
20 25 30  
Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
35 40 45  
Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
50 55 60  
Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
65 70 75 80  
Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
85 90 95  
Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr  
100 105 110  
Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu  
115 120 125  
His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn  
130 135 140  
Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr  
145 150 155 160  
Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser  
165 170 175  
Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met  
180 185 190  
Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr  
195 200 205  
Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe  
210 215 220

Asp	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	Cys
225					230					235					240
Tyr	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	Thr
				245					250					255	
Cys	Ala	Asp	Asn	Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	Thr	Thr
			260					265					270		
Glu	Cys	Ile	Gln	Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	Asn	Thr
		275					280					285			
Ile	Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	His
	290					295					300				
Glu	His	Asp	Met	Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	Arg	Glu
305					310					315					320
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ser	Pro	Trp	Cys	Phe	Thr
			325						330					335	
Thr	Asp	Pro	Asn	Ile	Arg	Val	Gly	Tyr	Cys	Ser	Gln	Ile	Pro	Asn	Cys
			340					345					350		
Asp	Met	Ser	His	Gly	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	Tyr
		355					360					365			
Met	Gly	Asn	Leu	Ser	Gln	Thr	Arg	Ser	Gly	Leu	Thr	Cys	Ser	Met	Trp
	370					375						380			
Asp	Lys	Asn	Met	Glu	Asp	Leu	His	Arg	His	Ile	Phe	Trp	Glu	Pro	Asp
385					390					395					400
Ala	Ser	Lys	Leu	Asn	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asp	Asp	Ala
				405					410					415	
His	Gly	Pro	Trp	Cys	Tyr	Thr	Gly	Asn	Pro	Leu	Ile	Pro	Trp	Asp	Tyr
			420					425					430		
Cys	Pro	Ile	Ser	Arg	Cys	Glu	Gly	Asp	Thr	Thr	Pro	Thr	Ile	Val	
		435					440						445		